## REMARKS

## STATUS OF THE CLAIMS:

Claims 1 to 40, 51 to 54 are cancelled.

Claims 41 to 50 and 55 to 60 are pending.

## I. Miscellaneous

### a. Objections to the Claims

The Examiner has objected to Claim 51 stating:

> Claim 51 is objected to under 37 CFR 1.75(c), as being of improper dependent form for failing to further limit the subject matter of a previous claim. Applicant is required to cancel the claim(s), or amend the claim(s) to place the claim(s) in proper dependent form, or rewrite the claim(s) in independent form. The polynucleotides of claim 51 are recited to be 95.0% identical to a polynucleotide sequence provided in claim 41, which in turn, recites polynucleotides encoding a polypeptide comprising amino acids 1-506 or 2-506 of SEQ ID NO:2. The polynucleotides of claim 41 are limited to the variants of SEQ ID NO: 1 permitted by the degeneracy of the genetic code. The polynucleotides of claim 52 are not so limited, however, because they are not required to code for a polypeptide. So, for example, a single C to A change at position 12 of SEQ ID NO: 1 would terminate translation; the resultant polynucleotide would meet all of the percent identity and hybridization limitations of claim 51 but would not encode either of the polypeptides recited in claim 41. Therefore, it would be possible to infringe claim 51 without infringing claim 41.

Applicants disagree with the Examiner's objection. However, in the sole interest of facilitating prosecution, Applicants have cancelled Claim 51. Accordingly, the Examiner's objection to Claim 51 has been rendered moot.

## II. Rejections under 35 U.S.C. § 112 – Second Paragraph

**a.** The Examiner has rejected Claims 51 and 52 under 35 U.S.C. § 112, second paragraph, alleging that these claims fail to comply with the written description requirement. More particularly, the Examiner states:

> Claims 51 and 52 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claims contain subject matter which was not described in the specification in such

a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention. The polynucleotides of claim 51 are recited to be 95.0% identical to a polynucleotide sequence provided in claim 41, which in turn, recites polynucleotides encoding a polypeptide comprising amino acids 1-506 or 2-506 of SEQ ID NO:2. While the polynucleotides of claim 41 are limited to the variants of SEQ ID NO: 1 permitted by the degeneracy of the genetic code, the polynucleotides of claim 52 are not so limited. Therefore, the genus of polynucleotides in claim 51 is described only by a partial structure in the form a percentage of sequence identity. There is not even identification of any particular portion of the structure that must be conserved. The hybridization limitation in the claim does not appreciably reduce the size of the encompassed genus, because all but the shortest oligonucleotides that are 95% identical to any portion of the reference sequence would hybridize under the recited conditions. Accordingly, in the absence of sufficient recitation of distinguishing identifying characteristics, the specification does not provide adequate written description of the claimed genus.

The polynucleotides of claim 52 encode a polypeptide that is at least 95.0% identical to SEQ ID NO:2. Thus, the claimed polynucleotides are not 95% identical to a limited set of described polynucleotides, but instead their variability is defined by the genus of encoded polypeptides. A full calculation of the number of unique polypeptides that are 95% identical to a 506 residue amino acid sequence is beyond the capability of the resources readily available to the examiner (Handheld calculators will not calculate intermediate values such as 506 factorial). However, the calculated number would be several orders of magnitude higher than 1.7 x 1016, which is the number of unique sequences that are 95% percent identical to a 100 amino acid sequence. This estimate only includes the 95% identity population--it ignores sequences of 94%, 93%, and etc. identity. It also ignores deletions that may preserve identity without substituting an amino acid. Therefore, Applicants' argument that the specification explicitly discloses over 52 or 54 individual species, i.e. 26 or 27 N-terminal and 26 or 27 C-terminal deletion mutants that are 95% identical to amino acids 2 to 506 or 1-506 of SEQ ID NO:2 is not persuasive with regard to description of the genus of polypeptides encompassed by the claim. Furthermore, although the specification establishes that HBMYP2X7v mRNA expression generally parallels that of P2X7, this does not define a function that could be coupled with sequence identity to describe variants of HBMYP2X7v polypeptides. Accordingly, in the absence of sufficient recitation of distinguishing identifying characteristics, the specification does not provide adequate

> written description of the genus of polypeptides recited in the claim. As the genus of encoded polypeptides is not described, the genus of encoding polynucleotides recited in claim 52 is likewise not described..

Applicants disagree with the Examiner's allegations. However, in the sole interest of facilitating prosecution, Applicants have cancelled Claims 51 and 52. Applicants believe the Examiner's rejection of Claims 51 and 52 under 35 U.S.C. § 112, second paragraph has been rendered moot.

**b.** The Examiner has rejected Claims 53 and 54 under 35 U.S.C. § 112, second paragraph, alleging that these claims fail to comply with the written description requirement. More particularly, the Examiner states:

> Claims 53 and 54 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention. The basis for this new matter rejection remains the same as it was applied to claims 33 and 34 in the previous office action. Applicants' arguments filed 02/15/2007 have been-fully considered but they are not persuasive. Applicants assert that the explicit disclosure of over 410 individual species (205 N-terminal deletion mutants and 205 C-terminal deletion mutants disclosed on pages 29 to 33) that encode a polypeptide "at least 302 contiguous amino acids of SEQ ID NO:2" or that is "at least 906 contiguous nucleotides of SEQ ID NO:I" is sufficient to constitute a representative number of species for the claimed genus. The question at hand is not whether the genus of polypeptides comprising at least 302 contiguous amino acids of SEQ ID NO:2 is described. Starting with SEQ ID NO:2, one of skill in the art can conceive all possible polypeptides that comprise at least 302 contiguous amino acids of SEQ ID NO:2. The skilled artisan can also conceive of all polypeptides comprising at least 301 contiguous amino acids, and all polypeptides comprising 303 amino acids, and so forth to any length over the entire sequence. Although the specification explicitly discloses of over 410 individual species of polypeptide that comprise at least 302 contiguous amino acids of SEQ ID NO:2, it also explicitly discloses an even greater number of individual species of polypeptide that comprise less than 302 contiguous amino acids

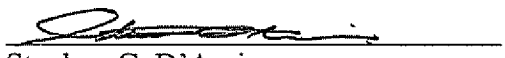
> of SEQ ID NO:2 (pages 29-33). The introduction of claim changes which involve narrowing the claims by introducing elements or limitations which are not supported by the as-filed disclosure is a violation of the written description requirement of 35 U.S.C. 112, first paragraph. See, e.g., Fujikawa v. Wattanasin, 93 F.3d 1559, 1571, 39 USPQ2d 1895, 1905 (Fed. Cir. 1996) (a "laundry list" disclosure of every possible moiety does not constitute a written description of every species in a genus because it would not "reasonably lead" those skilled in the art to any particular species). The specification as filed did not teach or suggest that the property of comprising at least 302 contiguous amino acids of SEQ ID NO:2 is critical or preferred, nor is this limitation found anywhere in the specification. The first mention of "at least 302 contiguous amino acids" occurred when it was introduced in the claim amendments filed 11/16/2006. Therefore, the limitations "at least 302 contiguous amino acids of SEQ ID NO:2" and "at least 906 contiguous nucleotides of SEQ ID NO: 1" are new matter not supported by the specification as filed.

Applicants disagree with the Examiner's allegations. However, in the sole interest of facilitating prosecution, Applicants have cancelled Claims 53 and 54. Applicants believe the Examiner's rejection of Claims 53 and 54 under 35 U.S.C. § 112, second paragraph has been rendered moot.

Applicants believe all of the Examiners rejections and objections have been overcome and that all of the pending claims before the Examiner are in condition for allowance. An early Office Action to that effect is, therefore, earnestly solicited.

If any fee is due in connection herewith not already accounted for, please charge such fee to Deposit Account No. 19-3880 of the undersigned. Furthermore, if any extension of time not already accounted for is required, such extension is hereby petitioned for, and it is requested that any fee due for said extension be charged to the above-stated Deposit Account.

Respectfully submitted,



Stephen C. D'Amico
Agent for Applicants
Reg. No. 46,652

Bristol-Myers Squibb Company
Patent Department
P.O. Box 4000
Princeton, NJ 08543-4000
(609) 252-5289

Date: 5-22-07